Author Contributions Checklist Form

This form documents the artifacts associated with the article (i.e., the data and code supporting the computational findings) and describes how to reproduce the findings.

Part 1: Data

☒ This paper **does not** involve analysis of external data (i.e., no data are used or the only data are generated by the authors via simulation in their code).

☒ I certify that the author(s) of the manuscript have legitimate access to and permission to use the data used in this manuscript.

Abstract

This projects invovles a simulation study which mimics phase I clinical trials. The data includes simulated dose-toxicity rates for 10,000 scenarios under different settings.

Availability

☒ Data **are** publicly available

☐ Data **cannot be made** publicly available

If the data are publicly available, see the *Publicly available data* section. Otherwise, see the *Non-publicly available data* section, below.

Publicly available data

☒ Data are available online at:
https://github.com/staceyfu1029/PoP-design/tree/main/JASA/skeleton_list

☐ Data are available as part of the paper's supplementary material.

☐ Data are publicly available by request, following the process described here:

☐ Data are or will be made available through some other mechanism, described here:

Non-publicly available data

Discussion of lack of publicly available data:

Description

File format(s)

☐ CSV or other plain text:
☐ Software-specific binary format (.Rda, Python pickle, etc.):
☐ Standardized binary format (e.g., netCDF, HDF5, etc.):
☒ Other (described here):

The dose-toxicity rates for 10,000 scenarios under different settings are provided in the “xlsx” files.

Data dictionary

☐ Provided by the authors in the following file(s):
☐ Data file(s) is (are) self-describiing (e.g., netCDF files)
☒ Available at the following URL:

https://github.com/staceyfu1029/PoP-design/blob/main/JASA/skeleton_list/Read.me

Additional information (optional)

Part 2: Code

Abstract

We provide codes that used to run the PoP, BOIN and Keyboard designs in our simulation study and the codes for visualizing the result in the GitHub repository.

Description

Code format(s)

☒ Script files
- ☒ R ☐ Python ☐ Matlab
- ☐ Other:

☐ Package
- ☐ R ☐ Python ☐ MATLAB toolbox
- ☐ Other:

☐ Reproducible report
- ☐ R Markdown ☐ Jupyter notebook
- ☐ Other:

☐ Shell script

☐ Other (described here):

Supporting software requirements

Version of primary software used

R version 4.3.0

Libraries and dependencies used by the code

BOIN, Keyboard, readxl, ggridges, ggplot2, viridis, hrbrthemes, gtable, grid, writexl

Supporting system/hardware requirements (optional)

Parallelization used

☒ No parallel code used
☐ Multi-core parallelization on a single machine/node
Number of cores used:
☐ Multi-machine/multi-node parallelization
Number of nodes and cores used:

License

☒ MIT License (default)
☐ BSD
☐ GPL v3.0
☐ Creative Commons
☐ Other (described here):

Additional information (optional)

Part 3: Reproducibility workflow

Scope

The provided workflow reproduces:

☐ Any numbers provided in text in the paper

☒ The computational method(s) presented in the paper (i.e., code is provided that implements the method(s))

☐ All tables and figures in the paper

☒ Selected tables and figures in the paper, as explained and justified here:

The provided codes can reproduce Figure 3, 4 and Table 2, 3 in the paper. Figure 1 and 2 are for illustration purpose and involve no data. Table 1 shows the decision boundaries that can be obtained using the function get_boundary from R package PoPdesign."

Workflow details

Location

The workflow is available:

☐ As part of the paper's supplementary material

☒ In this Git repository: https://github.com/staceyfu1029/PoP-design/tree/main/JASA

☐ Other:

Format(s)

☐ Single master code file

☐ Wrapper (shell) script(s)

☐ Self-contained R Markdown file, Jupyter notebook, or other literate programming approach

☒ Text file (e.g., a readme-style file) that documents workflow

☐ Makefile

☐ Other (more detail in 'Instructions' below)

Instructions

1. For Figure 3&4 or Table 2:

Step 1: simulate toxicity profiles
input the target toxicity phi and number of dose K in the code Skeleton_list.R. 10,000 scenarios will be generated.

Step 2: run simulations and save the output
run simulations for the simulated toxicity profiles. PoP, BOIN, Keyboard, and CRM designs can implemented using the corresponding codes that are provided in this GitHub repositories (PoP.R, BOIN. R, Keyboard.R, and CRM.R). R workspaces should be saved after running those R scripts to generate the figures and tables.

Step 3: generate figures and tables
with the outputs from step 2 for different simulation settings mentioned in the paper, table 2 can generated using the R script Table2.R. Figure 3 and 4 can be generated using the R script Figure3&4.R.

2. For Table 3:

Table 3 can be generated using the R script Table3.R

Expected run-time

Approximate time needed to reproduce the analyses on a standard desktop machine:
☐ <1 minute
☐ 1-10 minutes
☐ 10-60 minutes
☐ 1-8 hours
☒ >8 hours
☐ Not feasible to run on a desktop machine, as described here:

Additional documentation (optional)

Notes (optional)